BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

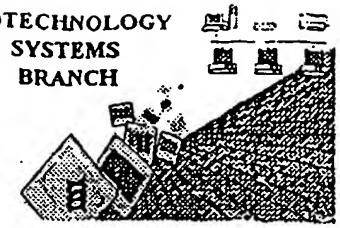
Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,096
Source: EFW0
Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: **TELEPHONE: 571-272-2510; FAX: 571-273-0221**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to **(EFFECTIVE 12/01/03)**: U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/798,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2____	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3____	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4__✓__	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5____	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6____	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7____	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8____	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. **If intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9____	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue n or Xaa represents.
10____	Invalid <213> Response	Per 1.823 of Sequence Rules, **the only valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
11____	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12____	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13____	Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

SEQUENCE LISTING

Submitted file could not be processe due to numerous erro

<110> Rea-Min Chu

Ching-Yi Lin

Ya-Wen Hsiao

Kuang-Wen Liao

mply with → pgs 1-4

<120> COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR CELLS

<160>4

<210>1

<211>636

<212>mRNA and PRT — delete, mandatory, <212> has to be either DNA, RNA OR PRT, IF it is both DNA/RNA please use type DNA and explain in sectio <220>-<223>. delete →

<213>Human — please insert <220>-<223>

<221>IL-6 — please insert into section <223>

<300>

<308>NCBI pubmed Genbank ; Accession No. : NM 000600 — Please insert dates for each accession No. [

<309> ← please insert, MAndatory, IF <308> is shown <309> must be inserte with resp

<400>1 — delete

63					78					93					108		
atg	aac	tcc	ttc	tcc	aca	agc	gcc	ttc	ggt	cca	gtt	gcc	tcc	tcc	ctg	ggg	ctg	ctc	ctg	60
Met	Asn	Ser	Phe	Ser	Thr	Ser	Ala	Phe	Gly	Pro	Val	Ala	Phe	Ser	Leu	Gly	Leu	Leu	Leu	
1				5					10					15					20	
123					138					153					168					
gtg	ttg	cct	gct	gcc	ttc	cct	gcc	cca	gta	ccc	cca	gga	gaa	gat	tcc	aaa	gat	gta	gcc	120
Val	Leu	Pro	Ala	Ala	Phe	Pro	Ala	Pro	Val	Pro	Pro	Gly	Glu	Asp	Ser	Lys	Asp	Val	Ala	
				25					30					35					40	
183					198					213					228					
gcc	cca	cac	aga	cag	cca	ctc	acc	tct	tca	gaa	cga	att	gac	aaa	caa	att	cgg	tac	atc	180
Ala	Pro	His	Arg	Gln	Pro	Leu	Thr	Ser	Ser	Glu	Arg	Ile	Asp	Lys	Gln	Ile	Arg	Tyr	Ile	
				45					50					55					60	
243					258					273					288					
ctc	gac	ggc	atc	tca	gcc	ctg	aga	aag	gag	aca	tgt	aac	aag	agt	aac	atg	tgt	gaa	agc	240
Leu	Asp	Gly	Ile	Ser	Ala	Leu	Arg	Lys	Glu	Thr	Cys	Asn	Lys	Ser	Asn	Met	Cys	Glu	Ser	
				65					70					75					80	
303					318					333					348					
agc	aaa	gag	gca	ctg	gca	gaa	aac	aac	ctg	aac	ctt	cca	aag	atg	gct	gaa	aaa	gat	gga	300
Ser	Lys	Glu	Ala	Leu	Ala	Glu	Asn	Asn	Leu	Asn	Leu	Pro	Lys	Met	Ala	Glu	Lys	Asp	Gly	
				85					90					95					100	
363					378					393					408					
tgc	ttc	caa	tct	gga	ttc	aat	gag	gag	act	tgc	ctg	gtg	aaa	atc	atc	act	ggt	ctt	ttg	360
Cys	Phe	Gln	Ser	Gly	Phe	Asn	Glu	Glu	Thr	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	
				105					110					115					120	
423					438					453					468					

← pleas see id # 4 on er Summa Shee

page 2

```
gag ttt gag gta tac cta cag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc      420
Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala
                125                 130                 135                 140

483                 498                 513                 528
aga gct gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca aag aat      480
Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
                145                 150                 155                 160

543                 558                 573                 588
cta gat gca ata acc acc cct gac cca acc aca aat gcc agc ctg ctg acg aag ctg cag      540
Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln
                165                 170                 175                 180

603                 618                 633                 648
gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg cgc agc ttt aag gag      600
Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
                185                 190                 195                 200

663                 678                 693
ttc ctg cag tcc agc ctg agg gct ctt cgg caa atg      636
Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
                205                 210
```

delete, see item #4 on error Summary sheet

<210>2

<211>60 — delete, same error

<212>mRNA and PRT — delete

<213>Human

<220> — please insert

<221>IL-2 Signal Peptide — please insert into section <223>.

<300>

<308>NCBI pubmed Genbank ; Accession No. : V00564 — same error

<309> — insert with response

<400>2

```
atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt      60
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
 1               5                  10                  15                  20
```

<210>3

<211>342 — delete, same error

<212>mRNA and PRT — delete

<213>Human

<220> — please insert

<221>Partial Sequence Encoding Human IL-15 — please move to section <223>.

<300>

<308>NCBI pubmed Genbank Accession No. : U14407 — same error

<3097 — pls insert

<400>3

```
aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat      60
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
1               5                  10                  15                  20

att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg     120
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
            25                  30                  35                  40

aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat     180
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
            45                  50                  55                  60

gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta     240
Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
            65                  70                  75                  80

aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg     300
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
            85                  90                  95                  100

cag agt ttt gta cat att gtc caa atg ttc atc aac act tct                          342
Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            105                 110
```

<210>4

<211>402 — delete, same error

<212>mRNA and PRT — delete — delete

<213> Artificial Chimeric Sequence — delete

<220>

<221>IL-2SP/IL-15MP — move to section <223>?

<223> Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP

<300>

<308>NCBI pubmed Genbank IL-2 Accession No. : V00564

IL-15 Accession No. : U14407

please insert dates for each accession No.

<3097 — insert

:400>4

```
atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt      60
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
1               5                  10                  15                  20
```

Sequence encoding IL-2signal peptide — delete

```
aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat     120
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
            25                  30                  35                  40
```

att gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg 180
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
45 50 55 60

aag tgc ttt ctc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat 240
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
65 70 75 80

gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta 300
Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
85 90 95 100

aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg 360
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
105 110 115 120

cag agt ttt gta cat att gtc caa atg ttc atc aac act tct 402
Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
125 130